

GenCore version 5.1.4.p5.4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 15, 2003, 15:07:49 ; Search time 16.7601 Seconds
(without alignments)
1537.035 Million cell updates/sec

Title: US-08-978-217-7
Perfect score: 445
Sequence: 1 NCALBELRLVFGPLGDLHA.....ELLDGQQAAPYHSGCAG 84

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 15338381 residues
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPRO.spool/US08978217/runat 14032003 141838 13457/app query.fasta_1.1500
-DB=issued_Patents_NA -QPM=faastac -SUBFIX=rni -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPMT=ptc -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_XLPRY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELEXT=7

Database :

1: Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	445	100.0	1920	1	US-08-746-789A-1
2	72	16.2	521	4	US-09-404-879A-139
3	72	16.2	551	4	US-09-404-879A-92
4	72	16.2	555	4	US-09-404-879A-107
5	72	16.2	2301	1	US-08-306-691B-23
6	72	16.2	2301	5	PCT-US93-06251-78
7	71.5	16.1	3141	2	US-08-956-242-1
8	71.5	16.1	3141	3	US-09-351-215-1
9	66.5	14.9	1473	4	US-09-518-914-7
10	66	14.8	1594	2	US-08-955-713-1
11	66	14.8	4154	1	US-08-131-365B-37
12	66	14.8	4154	2	US-08-668-123-37

C 13	65.5	14.7	111282	4	US-09-754-250-3	Sequence 3, Appl1
14	64.5	14.5	3546	1	US-08-162-809-9	Sequence 9, Appl1
15	64.5	14.5	3591	1	US-08-162-809-13	Sequence 19, Appl1
C 16	64.5	14.5	3807	1	US-08-357-598-1	Sequence 1, Appl1
C 17	64.5	14.5	3807	2	US-09-003-289-1	Sequence 1, Appl1
C 18	64.5	14.5	3807	5	PCT-US95-16435-1	Sequence 1, Appl1
19	64	14.4	32207	4	US-08-770-379-20	Sequence 20, Appl1
20	64	14.4	32207	2	US-08-757-669A-20	Sequence 20, Appl1
21	64	14.4	32207	4	US-09-230-371A-20	Sequence 20, Appl1
22	63.5	14.3	1575	4	US-09-134-001C-516	Sequence 516, App
23	63.5	14.3	3103	4	US-09-268-480-10	Sequence 10, Appl1
C 24	63	14.2	9997	1	US-08-246-982A-15	Sequence 15, Appl1
C 25	63	14.2	9997	1	US-08-453-265-15	Sequence 15, Appl1
C 26	63	14.2	10103	2	US-08-457-273B-7	Sequence 7, Appl1
C 27	62	13.9	3469	2	US-09-221-017B-106	Sequence 106, App
C 28	62	13.9	3854	2	US-08-720-484A-1	Sequence 1, Appl1
C 29	62	13.9	3854	3	US-08-953-823A-1	Sequence 1, Appl1
C 30	62	13.9	3854	4	US-09-398-239-1	Sequence 1, Appl1
C 31	62	13.9	6256	2	US-08-475-891A-1	Sequence 1, Appl1
C 32	62	13.9	6256	2	US-08-567-375-1	Sequence 1, Appl1
C 33	62	13.9	6256	2	US-08-587-680A-1	Sequence 1, Appl1
C 34	62	13.9	6846	4	US-08-961-527-198	Sequence 198, App
35	61.5	13.8	1263	4	US-08-811-481-31	Sequence 31, Appl1
36	61.5	13.8	2464	4	US-08-811-481-21	Sequence 21, Appl1
37	61.5	13.8	2943	2	US-08-548-159-2	Sequence 2, Appl1
38	61.5	13.8	2994	2	US-08-548-159-4	Sequence 4, Appl1
39	61.5	13.8	3777	3	US-09-121-321-15	Sequence 15, Appl1
40	61.5	13.8	3777	4	US-08-933-803A-15	Sequence 15, Appl1
41	61.5	13.8	5319	2	US-08-861-464-7	Sequence 7, Appl1
42	61.5	13.8	5319	2	US-08-396-001-7	Sequence 7, Appl1
43	61.5	13.8	5319	4	US-09-323-433A-7	Sequence 7, Appl1
C 44	61	13.7	477	4	US-08-465-380-35	Sequence 35, Appl1
C 45	61	13.7	477	2	US-08-486-397-35	Sequence 35, Appl1

ALIGNMENTS

RESULT 1
US-08-746-789A-1
; Sequence 1, Application US/08746789A
; Patent No. 5789200
; GENERAL INFORMATION:
; APPLICANT: Ismail Kola, Martin J. Tyms, Christine DeBuck
; TITLE OF INVENTION: A No. 5789200el Human ETS Family Member, ELF3
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: MICROSOFT WORD
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,789A
; FILING DATE: No. 5789200ember 15, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: William T. Han
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG 50024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270 5219
; TELEFAX: 610 270 4026
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

QY 81 CysGlyAla 83
Db 70 TGCCTTCA 62

RESULT 4
US-09-404-879A-107/C
; Sequence 107, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404, 879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 555
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-404-879A-107

Alignment Scores:
Pred. No.: 0.502 Length: 555
Score: 72.00 Matches: 31
Percent Similarity: 39.81% Conservative: 10
Best Local Similarity: 30.10% Mismatches: 32
Query Match: 16.18% Indels: 31
Gaps: 5

US-08-978-217-7 (1-84) x US-09-404-879A-107 (1-555)

QY 6 GluLeuArgLeuValPhe-----GlyProLeuGlyAspGlnLeuHisAlaGlnLeu 22
Db 358 GAGTTCATCTTTTCTTCATCTTTTAAGCCCGGTTTCAATACTTCATACCTCTCTC 299

QY 23 ArgAspLeuThrSerSerSerSerSerAspGluLeuSerTrpIleIleGluLeuLeuGly 42
Db 298 ACTCTCATCAACAGCTTTTTCAGC-----TTCTTCACAGCTTTTTCAGGCGC 254

QY 43 AspGlyMetAla-----PheGlnGlnAlaLeuAspProGly--- 54
Db 253 AGTGCCAGGCGCTCTGAGCAGGCTCCTTTTCAACAGCTGATCTTACGGTT 194

QY 55 -----ProPheAspGlnGlySerProPheAlaGlnGluLeuLeu 67
Db 193 CAAGGAGGCACTCAGCTCAGCTGTTCCGGGCGCGCTTTCCT-CAACTTCTC 135

QY 68 AspAspGlyGlnGlnAlaSerProGlyHis-----ProGlySer 80
Db 134 GCTGAGGCGCTCAGCTCTCTCTGATCATCTGCTGCTGCAAGAACTGGATCT 75

QY 81 CysGlyAla 83
Db 74 TGCCTTCA 66

RESULT 5
US-08-306-691B-23/C
; Sequence 23, Application US/08306691B
; Patent No. 5734039
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Skorski, Tomasz
; TITLE OF INVENTION: ANTISENSE
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
; STREET: Two Penn Center, Suite 1800

CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306, 691B
FILING DATE: September 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: No. 5734039e
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2301 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-08-306-691B-23

Alignment Scores:
Pred. No.: 3.39 Length: 2301
Score: 72.00 Matches: 31
Percent Similarity: 39.81% Conservative: 10
Best Local Similarity: 30.10% Mismatches: 32
Query Match: 16.18% Indels: 31
Gaps: 5

US-08-978-217-7 (1-84) x US-08-306-691B-23 (1-2301)

QY 6 GluLeuArgLeuValPhe-----GlyProLeuGlyAspGlnLeuHisAlaGlnLeu 22
Db 553 GAGTTCATCTTTTCTTCATCTTTTAAGCCCGGTTTCAATACTTCATACCTCTCTC 494

QY 23 ArgAspLeuThrSerSerSerSerSerAspGluLeuSerTrpIleIleGluLeuLeuGly 42
Db 493 ACTCTCATCAACAGCTTTTTCAGC-----TTCTTCAGCTTTTTCAGGCGC 449

QY 43 AspGlyMetAla-----PheGlnGlnAlaLeuAspProGly--- 54
Db 448 AGTGCCAGGCGCTCTGAGCAGGCTCCTTTTCAACAGCTGATCTTACGGTT 389

QY 55 -----ProPheAspGlnGlySerProPheAlaGlnGluLeuLeu 67
Db 388 CAAGGAGGCACTCAGCTCAGCTGTTCCGGGCGCGCTTTCCT-CAACTTCTC 330

QY 68 AspAspGlyGlnGlnAlaSerProGlyHis-----ProGlySer 80
Db 329 GCTGAGGCGCTCAGCTCTCTCTGATCATCTGCTGCTGCAAGAACTGGATCT 270

QY 81 CysGlyAla 83
Db 269 TGCCTTCA 261

RESULT 6
PCT-US93-06251-78/C
; Sequence 78, Application PC/TUS9306251
; GENERAL INFORMATION:
; APPLICANT: Wickstrom, Eric and Rife, Jason P.
; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates

```

; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06251
; FILING DATE: 19930630
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Digilio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2301 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US93-06251-78

Alignment Scores:
Pred. No.: 3.39 Length: 2301
Score: 72.00 Matches: 31
Percent Similarity: 39.81% Conservative: 10
Best Local Similarity: 30.10% Mismatches: 32
Query Match: 16.18% Indels: 31
DB: 5 Gaps: 5

US-08-978-217-7 (1-84) x PCT-US93-06251-78 (1-2301)
QY 6 GtLeuAArgLeuValPhe-----GlyProLeuGlyAspGlnLeuHisAlaGlnLeu 22
DB 553 GAGTTCATCTTTCTTCATCTTTTAAGCCGCGGTTTCAATAACCTCATACCTCTCTC 494
QY 23 ArgAspLeuThrSerSerSerSerAspGluLeuSerTrpIleIleGluLeuLeuGluLys 42
DB 493 ACTCTCATCAGCAGCTTTTTCAGC-----TTCTTCAGCTTTTGCAAGGC 449
QY 43 AspGlyMetAla-----PheGlnGluAlaLeuAspProGly--- 54
DB 448 AGTGGCCAGGCGCTCTGAGCAGGTCAGCTCTTTCACACAGCAGGATCTCAGCGTT 389
QY 55 -----ProPheAspGlnGlySerProPheAlaGlnGluLeu 67
DB 388 CAGAGAGCCACTCAGCTCAGCTCAGCTGCTCCGAGGCCGCTTTCTCCT-CAACTTCTC 330
QY 68 AspAspGlyGlnGlnAlaSerProTyrHis-----ProGlySer 80
DB 329 GCGGAGGCGCCTCAGCTCCTCTCTGCAATCATCTGCTGCTGCTGAGAACCTGATCT 270
QY 81 CyeGlyAla 83
DB 269 TCGGCTTCA 261

RESULT 7
US-08-956-242-1
; Sequence 1, Application US/08956242C
; Patent No. 5986081
; GENERAL INFORMATION:
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; APPLICANT: Ganetzky, Barry S.
; TITLE OF INVENTION: Titus, Steven A.
; FILE REFERENCE: Polynucleotides Encoding Herg-3
; CURRENT APPLICATION NUMBER: US/08/956,242C
; CURRENT FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3141
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (248)..(2128)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)
; OTHER INFORMATION: Unidentified at time of filing
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3)
; OTHER INFORMATION: Unidentified at time of filing
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (12)
; OTHER INFORMATION: Unidentified at time of filing
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1568)..(1872)
; OTHER INFORMATION: Unidentified at time of filing
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3126)
; OTHER INFORMATION: Unidentified at time of filing
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3134)
; OTHER INFORMATION: Unidentified at time of filing
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3141)
; OTHER INFORMATION: Unidentified at time of filing

Alignment Scores:
Pred. No.: 6.03 Length: 3141
Score: 71.50 Matches: 37
Percent Similarity: 37.17% Conservative: 5
Best Local Similarity: 32.74% Mismatches: 28
Query Match: 16.07% Indels: 44
DB: 2 Gaps: 5

US-08-978-217-7 (1-84) x US-08-956-242-1 (1-3141)
QY 9 LeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuAspLeuThrSerSer 28
DB 2227 CTGAAGCTGGGCTCCAGGCTAAGCAGCTCCAGGCCAGATAAACAGCTGAGTCCGC 2286
QY 29 SerSerAspGluLeuSerTrpIleIleGluLeuLeuLys-----AspGlyMet 45
DB 2287 GGTCTCTCAGACTCAGCCGCACTTGGAGCTCTCTCAAAACCCATGCCAGGGCCAC 2346
QY 46 Ala-----PheGln 48
DB 2347 GCCAGTACATCTGGAAGCCCTGCTCCCAATGACTGCTGCTGCTTCTAATAGCTCG 2406
QY 49 GluAlaLeuAspProGlyPro----- 55
DB 2407 GAGACGACGAGTCCAGGCGCAGGCTGCCCCAGGGCTTTCTCTCTGACACAGACCCA 2466
QY 56 -----PheAspGlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyGln 71
DB 2467 AGCTATGAGACTGTGATATCTGATCTCCAA-GCACAGAACTCTCTCC-----CAG 2519
QY 72 GlnAlaSerProTyrHisProGlySerCysGlyAlaGly 84
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Db 2520 GATGCTCACCCT-----GGCTGTGGCAACGGA 2546

RESULT 8

US-09-351-215-1

Sequence 1, Application US/09351215

Patent No. 6087488

GENERAL INFORMATION:

APPLICANT: Gametzky, Barry S.

APPLICANT: Titus, Steven A.

TITLE OF INVENTION: Polynucleotides Encoding Herg-3

FILE REFERENCE: 960296.94550

CURRENT APPLICATION NUMBER: US/09/351,215

CURRENT FILING DATE: 1999-07-12

EARLIER APPLICATION NUMBER: 08/956,242

EARLIER FILING DATE: 1997-10-22

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 3141

TYPE: DNA

ORGANISM: Homo sapien

FEATURE:

NAME/KEY: CDS

LOCATION: (246)..(2128)

FEATURE:

NAME/KEY: unsure

LOCATION: (1)

OTHER INFORMATION: Unidentified at time of filing

FEATURE:

NAME/KEY: unsure

LOCATION: (3)

OTHER INFORMATION: Unidentified at time of filing

FEATURE:

NAME/KEY: unsure

LOCATION: (12)

OTHER INFORMATION: Unidentified at time of filing

FEATURE:

NAME/KEY: unsure

LOCATION: (3126)

OTHER INFORMATION: Unidentified at time of filing

FEATURE:

NAME/KEY: unsure

LOCATION: (3134)

OTHER INFORMATION: Unidentified at time of filing

US-09-351-215-1

Alignment Scores:

Pred. No.: 6.03 Length: 3141

Score: 71.50 Matches: 37

Percent Similarity: 37.17% Conservative: 5

Best Local Similarity: 32.74% Mismatches: 28

Query Match: 16.07% Indels: 44

DB: 3 Gaps: 5

US-08-978-217-7 (1-84) x US-09-351-215-1 (1-3141)

Qy 9 LeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSerSer 28

Db 2227 CTGAAGCTGGGCTCCAGGCTAGACGACCTCCAGCCAGATGAACAGGTGAGTCCGCC 2286

Qy 29 SerSerAspGlnLeuSerTrpIleIleGlnLeuLeuGlnLys-----AspGlyMet 45

Db 2287 GTGTCCTCAGACCTCAGCGCATCTTGAGCTCTCCAGAACCCATGCCCGGCGCAC 2346

Qy 46 Ala-----PheGln 48

Db 2347 GCCAGCTACATTTCTGGAAGCCCTCCCTCCAAATGACCTGGCTTGCTTATGACCTCG 2406

Qy 49 GluAlaLeuAspProGlyPro----- 55

Db 2407 GAGACGACGAGTCCAGGCGCCAGGCTGCCCCGCTTTCTGCTTCTGACAGACCCCA 2466

Qy 56 -----PheAspGlnGlySerProPheAlaGlnGlnLeuLeuAspGlyGln 71

Db 2467 AGCTATGAGACTTGATGATGACTGTGTCCTCAAA-GCACAGAACTCTCTCC-----CAG 2519

Qy 72 GluAlaSerProTyRHisProGlySerCysGlyAlaGly 84

Db 2520 GATGCTCACCCT-----GGCTGTGGCAACGGA 2546

RESULT 9

US-09-518-914-7

Sequence 7, Application US/09518914

Patent No. 6413731

GENERAL INFORMATION:

APPLICANT: Borowsky, Beth E.

APPLICANT: Ogozalek, Kristine L.

APPLICANT: Lakhiani, Parul P.

TITLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS

FILE REFERENCE: 59138-A/CPM

CURRENT APPLICATION NUMBER: US/09/518,914

EARLIER APPLICATION NUMBER: 2000-03-03

EARLIER FILING DATE: 1999-05-03

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 7

LENGTH: 1473

TYPE: DNA

ORGANISM: Rattus norvegicus

US-09-518-914-7

Alignment Scores:

Pred. No.: 10.4 Length: 1473

Score: 66.50 Matches: 26

Percent Similarity: 36.84% Conservative: 9

Best Local Similarity: 27.37% Mismatches: 31

Query Match: 14.94% Indels: 29

DB: 4 Gaps: 4

US-08-978-217-7 (1-84) x US-09-518-914-7 (1-1473)

Qy 7 LeuArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeu----- 22

Db 1117 CTGGGGGTCTTCTTGAGATATCAAGCCAGCGACCACTCCCTCCTAGCTACCGCTCT 1176

Qy 23 -----ArgAspLeuThrSerSerSerSerAspGlnLeuSerTrpIleIleGlnLeu 40

Db 1177 ACCATCGCTCCACACTGACAGCAGCTCTCAGACCTCAGCTGATC----- 1224

Qy 41 GluIysAspGlyMetAlaPheGlnGlnAlaLeu-----AspProGlyProPhe 56

Db 1225 -----TCTGGGCGAAGCGCCAGAGTCTCTGGGTCTGAGAGTGAAGTGGGTGACA 1278

Qy 57 Asp-----GlnGlySerProPheAla 63

Db 1279 GACACAGAAACACAGCTGCTGGGAGCTGCCAGACGAAGTGAATCTTCTGTC 1338

Qy 64 GlnGlnLeuLeuAspAspGlyGlnGlnAlaSerProTyRHisPro 78

Db 1339 AGTATGACCTGGAAGATGAGAAATCAAGCTCTTCCACCCCC 1383

RESULT 10

US-08-955-713-1/c

Sequence 1, Application US/08955713

Patent No. 5955308

GENERAL INFORMATION:

APPLICANT: SATHE, GANESH

APPLICANT: MOONEY, JEFFREY

APPLICANT: BERGMA, DERK-

APPLICANT: HALSEY, WENDY

```

      TITLE OF INVENTION:  CDNA CLONE HEAD54 THAT ENCODES
NUMBER OF SEQUENCES:    4
CORRESPONDENCE ADDRESS:
ADDRESSEE:  RAINIER & PRESTIA
STREET:    P.O. BOX 980
CITY:      VALLEY FORGE
STATE:     PA
COUNTRY:   USA
ZIP:       19482

COMPUTER READABLE FORM:
MEDIUM TYPE:  Diskette
COMPUTER:     IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE:     FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,713
FILING DATE:      23-OCT-1997
CLASSIFICATION:   435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050,124
FILING DATE:      18-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME:             PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70087
TELECOMMUNICATION INFORMATION:
TELEPHONE:        610-407-0700
TELEFAX:          610-407-0701
TELEX:            846169

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH:           1594 base pairs
TYPE:              nucleic acid
STRANDEDNESS:     single
TOPOLOGY:         linear
MOLECULE TYPE:    CDNA
US-08-955-713-1

Alignment Scores:
Pred. NO.:        13.5                Length:      1594
Score:            66.00               Matches:     27
Percent Similarity: 36.96%            Conservative: 7
Best Local Similarity: 29.35%         Mismatches:  36
Query Matchn:     14.83%              Indels:      22
DB:               2                  Gaps:         4

US-08-978-217-7 (1-84) x US-08-955-713-1 (1-1594)

QY      12  GLYProlenGlyAAspGlInLeuHlaIagInLeuArg-----AAspLeu 25
Db      1114 GCCCTTCGGCGGGCTGTGCCTGCCCCAGACCAACGCGTTCCGATGGTGAACCCACTGCT 1055
                                     ::::
QY      26  ThrSerSerSerSerAspGluLeuSerTryptileIleGluLeuGlnLysAAsp----- 43
Db      1054 CACAATAGCAAAGAGATGAGCGGCCAGTAGTGCGCAGAAGAACTCACAGACGTAACAAGCTG 995
                                     ::::
QY      44  -----GlyMetAlaPheGlnGlnAlaLeuAAspProGlyProPhe 56
Db      994 GTGCCAGCGAGCGAGCGCGAGGGGCTTGCGCCACCCTGTAGCTGAGGCGAGAGGGGCC 935
                                     ::::
QY      57  AAspGlnGlySerProPheAlaGlnGluLeuLeu-----AAspAAspGlyGlnGln 72
Db      934 GGAGAAAGG-----GCTTCAGAGAGAGAGTGCCCCGTTGAGAGAGACAGATGCCACC 884
                                     ::::
QY      73  AlaSerProTyRHisProGlySerCyseGlyAlaGly 84
Db      883 GAGTCCCCCGGCGCACCCGGGCAAGCTGCCCCCCCACGGA 848

RESULT 11
US-08-131-365B-37
; Sequence 37, Application US/08131365B
; Patent No. 5527690
; GENERAL INFORMATION:

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1  APPLICANT: Brown, Michael S.
2  APPLICANT: Brown, Michael R.
3  APPLICANT: Wang, Xiaodong
4  APPLICANT: Goldstein, Joseph L.
5  TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
6  TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING
7  TITLE OF INVENTION: PROTEINS
8  NUMBER OF SEQUENCES: 64
9  CORRESPONDENCE ADDRESS:
10 ADDRESSER: Arnold, White & Durkee
11 STREET: P.O. Box 4433
12 CITY: Houston
13 STATE: Texas
14 COUNTRY: U.S.A.
15 ZIP: 77210
16
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: PatentIn Release #1.0, Version #1.30
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/131,365B
24 FILING DATE: 01-OCT-1993
25 CLASSIFICATION: 435
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Parker, David L.
28 REGISTRATION NUMBER: 32,165
29 REFERENCE/DOCKET NUMBER: UTSID:372/PAR
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: (512) 418-3000
32 TELEFAX: (512) 474-7577
33 INFORMATION FOR SEQ. ID NO: 37:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 4154 base pairs
36 TYPE: nucleic acid
37 STRANDEDNESS: single
38 TOPOLOGY: linear
39 MOLECULE TYPE: other nucleic acid
40 DESCRIPTION: /desc = "DNA"
41
42 FEATURE:
43 NAME/KEY: CDS
44 LOCATION: 167..3607
45
46 US-08-111-365B-37
47
48 Alignment Scores:
49 Pred. No.: 49 Length: 4154
50 Score: 66.00 Matches: 21
51 Percent Similarity: 47.62% Conservative: 9
52 Best Local Similarity: 33.33% Mismatches: 23
53 Query Match: 14.83% Indels: 10
54 DB: 1 Gaps: 2
55
56 US-08-978-217-7 (1-84) x US-08-111-365B-37 (1-4154)
57
58 QY 22 LeuAAGAspleuThrSerSerSerSerAspGluLeuSerTrpIleIleGluLeuGlu 41
59 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
60 DB 1355 CTGAAGGATCTGCGTGGCTGCGCTGCGCACTGAGGAGGAAACACAGACTG---CTATGAG 1411
61 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
62 QY 42 LysAspGlyMetAlaPheGlnGlnAlaLeuAspProGlyProPheAspGlnGlySerPro 61
63 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
64 DB 1412 GAGCGAAGACCTGAGCGAGACACACCTGACCCCACTCGGAGATGCTGCTACCT 1471
65 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
66 QY 62 PheAlaGlnGluLeuLeuAspAspGlyGlnGlnAlaSerProTyrHisProGlySerCys 81
67 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
68 DB 1472 TTC-----CAGAGCAGCCCTTGTCTCCCTTGGCAGCAG 1504
69 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
70 QY 82 GlyAlaGly 84
71 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
72 DB 1505 GGCAGGTGC 1513
73 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
74
75 RESULT 12
76 US-08-668-123-37
77 / Sequence 37, Application US/08668123

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,809
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3546 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 2..2920
US-08-162-809-9

Alignment Scores:
Pred. No.: 63.3 Length: 3546
Score: 64.50 Matches: 22
Percent Similarity: 43.42% Conservative: 11
Best Local Similarity: 28.95% Mismatches: 38
Query Match: 14.49% Indels: 6
DB: 1 Gaps: 1

US-08-978-217-7 (1-84) x US-08-162-809-9 (1-3546)

QY 13 ProLeuGlyAAspGlnLeuHisAlaGlnLeuArgAspLeuThrSerSerSerAAspGlu 32
DB 2170 CCTCTAGAGATGAACTAGCTGACCGAGACCTGG-CTGCCCGCAACATCTGTCACACA 2228

QY 33 LeuSerTrpIleIleGluLeuLeuGluLyAAspGlyMetAlaPheGlnGluAlaLeuAsp 52
DB 2229 GCACTTGTCTGCAAGTCTGACTTCGGGCTCCCGCTTTTGGAGGATGATCCAG 2288

QY 53 -----ProGlyProPheAspGlnGlySerProPheAlaGlnGluLeu 67
DB 2289 CCGACCCCACTACACAGCTCCCTGGGAGCAAGATCCCATCAGGTGAGACGCTCTG 2348

QY 68 AspAspGlyGlnGlnAlaSerProTyrHisProGlySerCyAGlyAla 83
DB 2349 AGGCGATCGCTTACCGCAATTCACTCGGCCACGACGATGTGAGCT 2396

RESULT 15
US-08-162-809-13
Sequence 13, Application US/08162809
Patent No. 5457046
GENERAL INFORMATION:
APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoon G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,809
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 3591 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 2..2965
US-08-162-809-13

Alignment Scores:
Pred. No.: 64.4 Length: 3591
Score: 64.50 Matches: 22
Percent Similarity: 43.42% Conservative: 11
Best Local Similarity: 28.95% Mismatches: 38
Query Match: 14.49% Indels: 6
DB: 1 Gaps: 1

US-08-978-217-7 (1-84) x US-08-162-809-13 (1-3591)

QY 13 ProLeuGlyAAspGlnLeuHisAlaGlnLeuArgAspLeuThrSerSerSerAAspGlu 32
DB 2215 CCTCTAGAGATGAACTAGCTGACCGAGACCTGG-CTGCCCGCAACATCTGTCACACA 2273

QY 33 LeuSerTrpIleIleGluLeuLeuGluLyAAspGlyMetAlaPheGlnGluAlaLeuAsp 52
DB 2274 GCACTTGTCTGCAAGTCTGACTTCGGGCTCCCGCTTTTGGAGGATGATCCAG 2333

QY 53 -----ProGlyProPheAspGlnGlySerProPheAlaGlnGluLeu 67
DB 2334 CCGACCCCACTACACAGCTCCCTGGGAGCAAGATCCCATCAGGTGAGACGCTCTG 2393

QY 68 AspAspGlyGlnGlnAlaSerProTyrHisProGlySerCyAGlyAla 83
DB 2394 AGGCGATCGCTTACCGCAATTCACTCGGCCACGACGATGTGAGCT 2441

Search completed: March 15, 2003, 23:33:00
Job time : 36.7601 secs

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